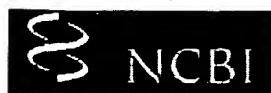


Exhibit C



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

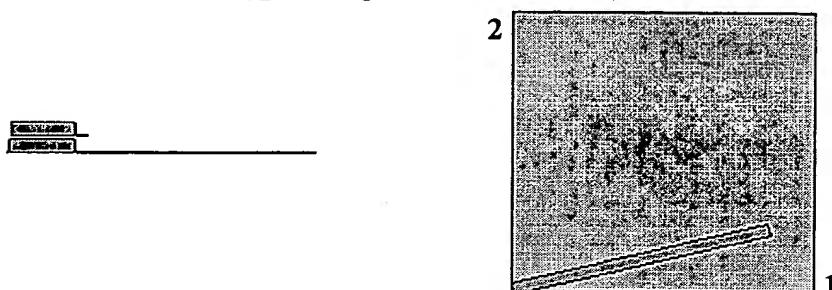
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.6 [Apr-09-2003]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2
 x_dropoff: 50 expect: 10.00000 wordsize: 11 Filter Align

Sequence 1 lcl|seq_1 Length 1414 (1 .. 1414)

Sequence 2 lcl|seq_2 Length 5540 (1 .. 5540)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 2286 bits (1189), Expect = 0.0
 Identities = 1191/1192 (99%)
 Strand = Plus / Plus

 SEQ ID NO: 1 AF279145

Query: 1 aggacccgcgaggaaggggcccgcggatggcgcgtccctgagggtcgtaggcgagttcgccg 60
 Sbjct: 41 aggacccgcgaggaaggggcccgcggatggcgcgtccctgagggtcgtaggcgagttcgccg 100

Query: 61 agcgtggaaaggagcggaccctgctctcccccggctgcggccatggccacggcggagcg 120
 Sbjct: 101 agcgtggaaaggagcggaccctgctctcccccggctgcggccatggccacggcggagcg 160

Query: 121 gagagccctcgcatcggttccagtggctctttggccactctgggtcatctgcgc 180
 Sbjct: 161 gagagccctcgcatcggttccagtggctctttggccactctgggtcatctgcgc 220

Query: 181 cggcaaggggacgcaggagatgggggtccagcctgctacggcggattgacctgta 240
 Sbjct: 221 cggcaaggggacgcaggagatgggggtccagcctgctacggcggattgacctgta 280

Query: 241 cttcatttggacaaatcaggaagtgtgctgcaccactggaatgaaatctattactttgt 300
Sbjct: 281 cttcatttggacaaatcaggaagtgtgctgcaccactggaatgaaatctattactttgt 340

Query: 301 ggaacagttggctcacaaattcatcagcccacagttgagaatgtccttattgtttctc 360
Sbjct: 341 ggaacagttggctcacaaattcatcagcccacagttgagaatgtccttattgtttctc 400

Query: 361 cacccgaggaacaacctaataatgaaactgacagaagacagagaacaaatccgtcaaggcct 420
Sbjct: 401 cacccgaggaacaacctaataatgaaactgacagaagacagagaacaaatccgtcaaggcct 460

Query: 421 agaagaactccagaaagttctgccaggaggagacacttacatgcatgaaggattgaaag 480
Sbjct: 461 agaagaactccagaaagttctgccaggaggagacacttacatgcatgaaggattgaaag 520

Query: 481 ggccagtgagcagattattatgaaaacagacaagggtacaggacagccagcgtcatcat 540
Sbjct: 521 ggccagtgagcagattattatgaaaacagacaagggtacaggacagccagcgtcatcat 580

Query: 541 tgctttgactgatggagaactccatgaagatctctttctattcagagagggaggctaa 600
Sbjct: 581 tgctttgactgatggagaactccatgaagatctctttctattcagagagggaggctaa 640

Query: 601 taggtctcgagatcttggtcaattgttactgtgttgtgtgaaagattcaatgagac 660
Sbjct: 641 taggtctcgagatcttggtcaattgttactgtgttgtgtgaaagattcaatgagac 700

Query: 661 acagctggcccgattgcggacagtaaggatcatgtgttcccgtaatgacggcttc 720
Sbjct: 701 acagctggcccgattgcggacagtaaggatcatgtgttcccgtaatgacggcttc 760

Query: 721 ggctctgcaaggcatcatccactcaatttgaagaagtgcctgcattcgaaattctagcgc 780
Sbjct: 761 ggctctgcaaggcatcatccactcaatttgaagaagtgcctgcattcgaaattctagcgc 820

Query: 781 tgaaccatccaccatatgtcaggagagtcatcaagttgtcgtagagggaaacggctt 840
Sbjct: 821 tgaaccatccaccatatgtcaggagagtcatcaagttgtcgtagagggaaacggctt 880

Query: 841 ccgacatgcccgaacgtggacagggtcctctgcagctcaagatcaatgactcggtcac 900
Sbjct: 881 ccgacatgcccgaacgtggacagggtcctctgcagctcaagatcaatgactcggtcac 940

Query: 901 actcaatgagaagccctttctgtgaaagacacttattactgtgtccagcgcctatctt 960
Sbjct: 941 actcaatgagaagccctttctgtgaaagacacttattactgtgtccagcgcctatctt 1000

Query: 961 aaaagaagttggcatgaaagctgcactccaggcagcatgaacatggcctcttttat 1020
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1001 aaaagaagttggcatgaaagctgcactccaggcagcatgaacatggcctcttttat 1060

Query: 1021 ctccagttctgtcatcatcaccaccacactgttctgacgggtccatcctggccatcgc 1080
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1061 ctccagttctgtcatcatcaccaccacactgttctgacgggtccatcctggccatcgc 1120

Query: 1081 cctgctgatcctgttcctgctccatggcttcctctgggtctggccctctg 1140
||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1121 cctgctgatcctgttcctgctccatggcttcctctgggtctggccctctg 1180

Query: 1141 ctgcactgtgattatcaaggaggccctccacccctgccgaggagagttag 1192
||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1181 ctgcactgtgattatcaaggaggccctccacccctgccgaggagagttag 1232

CPU time: 0.01 user secs. 0.02 sys. secs 0.03 total secs.

Lambda K H
1.33 0.621 1.12

Gapped

Lambda K H
1.33 0.621 1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 8
Number of Sequences: 0
Number of extensions: 8
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 1414
length of database: 10,224,276,066
effective HSP length: 25
effective length of query: 1389
effective length of database: 10,224,276,041
effective search space: 14201519420949
effective search space used: 14201519420949
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 21 (41.1 bits)